

SEQUENCE LISTING

<110> Dhugga, Kanwarpal S.
Niu, Xiaomu
Helentjaris, Timothy

<120> Manipulation of Sucrose Synthase Genes
to Improve Stalk and Grain Quality

<130> 1301

<150> 60/270,777

<151> 2001-02-22

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2737

<212> DNA

<213> Zea mays

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cgagcagctc acagctctcg agtacctccg cttcaaggag gagcttgctg acggccagca	360
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<212> PRT
<213> Zea mays

<400> 2

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35 40 45
Gly Ser Gly Gly Arg Ala Leu Ala Glu Gly Pro Phe Leu Asp Val Leu
50 55 60
Arg Ser Ala Gln Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile Ala
65 70 75 80
Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His
85 90 95
Glu Leu Ser Val Glu Gln Leu Thr Val Ser Glu Tyr Leu Arg Phe Lys
100 105 110
Glu Glu Leu Val Asp Gly Gln His Asn Asp Pro Tyr Val Leu Glu Leu
115 120 125
Asp Phe Glu Pro Phe Asn Val Ser Val Pro Arg Pro Asn Arg Ser Ser
130 135 140
Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Ile
145 150 155 160
Met Phe Arg Asn Arg Asp Cys Leu Glu Pro Leu Leu Asp Phe Leu Arg
165 170 175
Gly His Arg His Lys Gly His Val Met Met Leu Asn Asp Arg Ile Gln
180 185 190
Ser Leu Gly Arg Leu Gln Ser Val Leu Thr Lys Ala Glu Glu His Leu
195 200 205
Ser Lys Leu Pro Ala Asp Thr Pro Tyr Ser Gln Phe Ala Tyr Lys Phe
210 215 220
Gln Glu Trp Gly Leu Glu Lys Gly Trp Gly Asp Thr Ala Gly His Val
225 230 235 240
Leu Glu Met Ile His Leu Leu Leu Asp Ile Ile Gln Ala Pro Asp Pro
245 250 255
Ser Thr Leu Glu Lys Phe Leu Gly Arg Ile Pro Met Ile Phe Asn Val
260 265 270
Val Val Val Ser Pro His Gly Tyr Phe Gly Gln Ala Asn Val Leu Gly
275 280 285
Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln Val Arg

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290	295	300
Ala Leu Glu Asn Glu Met Val Leu Arg Leu Lys Lys Gln Gly Leu Asp		
305	310	315
Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys		
	325	330
Gly Thr Ser Cys Asn Gln Arg Leu Glu Arg Ile Ser Gly Thr Gln His		
	340	345
Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys		
	355	360
Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala		
	370	375
Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro Asp		
385	390	395
Phe Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu		
	405	410
Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His Ala Leu Glu		
	420	425
Lys Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu		
	435	440
Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Ile Ile Ala Met Asn		
	450	455
Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser		
465	470	475
Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro		
	485	490
Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe		
	500	505
Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr		
	515	520
Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu		
	530	535
Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp		
545	550	555
Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys		
	565	570
Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg		
	580	585
Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn Asp Val Asn Lys		
	595	600
Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu		
	610	615
Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln		
625	630	635
Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr		
	645	650
His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr		
	660	665
Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His		
	675	680
Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile		
	690	695
Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe		
705	710	715
Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala		
	725	730
Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu		
	740	745
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser		

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755 760 765
 Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ile
 770 775 780
 Leu Lys Phe Arg Glu Leu Ala Lys Thr Val Pro Leu Ala Ile Asp Gln
 785 790 795 800
 Pro Gln

<210> 3
 <211> 36
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 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon the adapter
 sequence and poly T to remove clones which have a
 poly A tail but no cDNA.

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<210> 4
 <211> 2746
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (72) ... (2480)

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 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu
 1 5 10

 cgc ctt ggt gcc acc ttc tcc tcc cat ccc aat gaa ctg ata gca ctc 158
 Arg Leu Gly Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu
 15 20 25

 ttt tcc agg tat gtt cac cag ggc aag gga atg ctt cag cgc cat cag 206
 Phe Ser Arg Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln
 30 35 40 45

 ctg ctt gcg gag ttt gat gcc ctg ttt gat agt gac aag gag aag tat 254
 Leu Leu Ala Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr
 50 55 60

 gca cca ttt gaa gac att ctt cgt gct gct cag gaa gca att gtg ctc 302
 Ala Pro Phe Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu
 65 70 75

 ccc cca tgg gtt gca ctt gct atc agg cca agg cct ggt gtc tgg gat 350
 Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp
 80 85 90

 tac att cgg gtg aat gta agt gag ctg gct gtg gag gag ctg agt gtt 398

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Tyr	Ile	Arg	Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Ser	Val		
95						100					105						
tct	gag	tac	ttg	gca	ttc	aag	gaa	cag	ctg	gtg	gat	gga	caa	tcc	aac	446	
Ser	Glu	Tyr	Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Gly	Gln	Ser	Asn		
110					115					120					125		
agc	aac	ttt	gtg	ctt	gag	ctt	gat	ttt	gag	ccc	ttc	aat	gcc	tcc	ttt	494	
Ser	Asn	Phe	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe		
				130					135					140			
cct	cgt	cct	tcc	atg	tcg	aag	tcc	atc	gga	aat	gga	gtg	caa	ttc	ctt	542	
Pro	Arg	Pro	Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu		
			145					150					155				
aac	cga	cac	ctg	tcg	tcc	aag	ttg	ttc	cag	gac	aag	gag	agt	ttg	tac	590	
Asn	Arg	His	Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Lys	Glu	Ser	Leu	Tyr		
		160					165					170					
ccc	ttg	ctg	aac	ttc	ctc	aag	gct	cat	aac	tac	aag	ggc	acg	acg	atg	638	
Pro	Leu	Leu	Asn	Phe	Leu	Lys	Ala	His	Asn	Tyr	Lys	Gly	Thr	Thr	Met		
	175					180					185						
atg	ttg	aat	gac	aga	atc	caa	agc	ctt	cgt	ggc	ctc	caa	tca	tcc	ctg	686	
Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ser	Leu		
190					195					200					205		
aga	aag	gca	gag	gag	tat	cta	ctg	agt	ggt	cct	caa	gac	act	ccc	tac	734	
Arg	Lys	Ala	Glu	Glu	Tyr	Leu	Leu	Ser	Val	Pro	Gln	Asp	Thr	Pro	Tyr		
				210					215					220			
tcg	gag	ttc	aac	cat	agg	ttc	caa	gag	ctt	ggc	ttg	gag	aag	ggc	tgg	782	
Ser	Glu	Phe	Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp		
			225				230						235				
ggc	gac	act	gag	aag	cgt	ggt	ctc	gac	aca	ctc	cac	ttg	ctt	ctc	gac	830	
Gly	Asp	Thr	Ala	Lys	Arg	Val	Leu	Asp	Thr	Leu	His	Leu	Leu	Leu	Asp		
		240				245						250					
ctt	ctt	gag	gcc	cct	gat	cct	gcc	aac	ttg	gag	aag	ttc	ctt	gga	act	878	
Leu	Leu	Glu	Ala	Pro	Asp	Pro	Ala	Asn	Leu	Glu	Lys	Phe	Leu	Gly	Thr		
		255				260					265						
ata	cca	atg	atg	ttc	aac	ggt	ggt	atc	ctg	tct	cct	cat	ggc	tac	ttc	926	
Ile	Pro	Met	Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe		
270					275					280					285		
gcc	cag	tcc	aat	gtg	ctt	gga	tac	cct	gac	act	ggc	ggc	cag	ggt	gtg	974	
Ala	Gln	Ser	Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val		
				290					295				300				
tac	att	ctg	gat	caa	gtc	cgt	gct	ttg	gag	aat	gag	atg	ctt	ctg	agg	1022	
Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg		
			305					310					315				
att	aag	cag	caa	ggc	ctt	gat	atc	act	ccg	aag	atc	ctc	att	ggt	acc	1070	
Ile	Lys	Gln	Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr		
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aag gtc att ggt act gag cac aca gac atc att cgc gtt ccc ttc aga Lys Val Ile Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg 350 355 360 365	1166
aat gag aat ggc atc ctc cgc aag tgg atc tct cgt ttt gat gtc tgg Asn Glu Asn Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp 370 375 380	1214
cca tac ctg gag aca tac act gag gat gtt tcc agt gaa ata atg aaa Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys 385 390 395	1262
gaa atg cag gcc aag cct gac ctt atc att ggc aac tac agc gat ggc Glu Met Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly 400 405 410	1310
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acc atc gct cat gcc ttg gag aaa acc aaa tac ccc aac tcg gac atc Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile 430 435 440 445	1406
tac ttg gac aaa ttc gac agc cag tac cac ttc tct tgc cag ttc aca Tyr Leu Asp Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr 450 455 460	1454
gct gac ctt att gcc atg aac cac acc gat ttc atc atc acc agc aca Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr 465 470 475	1502
ttc caa gaa atc gcg gga agc aag gac acc gtg ggg cag tac gag tcc Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser 480 485 490	1550
cat atc gcg ttc act ctt cct ggg ctc tac cgt gtc gtc cat ggc atc His Ile Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile 495 500 505	1598
gat gtt ttc gat ccc aag ttc aac att gtc tct cct gga gca gac atg Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met 510 515 520 525	1646
agt gtt tac tac cct tat acg gaa acc gac aag aga ctc act gcc ttc Ser Val Tyr Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe 530 535 540	1694
cat cct gaa atc gag gag ctc atc tac agc gac gtc gag aac tcc gag His Pro Glu Ile Glu Glu Leu Ile Tyr Ser Asp Val Glu Asn Ser Glu 545 550 555	1742
cac aag ttc gtg ctg aag gac aag aag aag ccg atc atc ttc tcg atg	1790

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His	Lys	Phe	Val	Leu	Lys	Asp	Lys	Lys	Lys	Pro	Ile	Ile	Phe	Ser	Met		
		560					565					570					
gcg	cgt	ctc	gac	cg	gtg	aag	aac	atg	aca	ggc	ctg	gtc	gag	atg	tac	1838	
Ala	Arg	Leu	Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Tyr		
	575					580					585						
ggc	aag	aac	gcg	cg	ctg	agg	gag	ctg	gcg	aac	ctc	gtg	atc	gtt	gcc	1886	
Gly	Lys	Asn	Ala	Arg	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala		
590					595					600					605		
ggt	gac	cac	ggc	aag	gag	tcc	aag	gac	agg	gag	gag	cag	gcg	gag	ttc	1934	
Gly	Asp	His	Gly	Lys	Glu	Ser	Lys	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Phe		
			610						615					620			
aag	aag	atg	tac	agc	ctc	atc	gac	gag	tac	aag	ttg	aag	ggc	cat	atc	1982	
Lys	Lys	Met	Tyr	Ser	Leu	Ile	Asp	Glu	Tyr	Lys	Leu	Lys	Gly	His	Ile		
			625					630						635			
cg	tgg	atc	tgc	gcg	cag	atg	aac	cgt	gtc	cg	aac	ggg	gag	ctg	tac	2030	
Arg	Trp	Ile	Ser	Ala	Gln	Met	Asn	Arg	Val	Arg	Asn	Gly	Glu	Leu	Tyr		
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cg	tac	att	tgc	gat	acc	aag	ggc	gca	ttc	gtg	cag	cct	gcg	ttc	tac	2078	
Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Phe	Tyr		
	655					660					665						
gaa	gcg	ttc	ggc	ctg	act	gtg	atc	gag	tcc	atg	acg	tgc	ggc	ctg	cca	2126	
Glu	Ala	Phe	Gly	Leu	Thr	Val	Ile	Glu	Ser	Met	Thr	Cys	Gly	Leu	Pro		
670					675					680					685		
acg	atc	gcg	acc	tgc	cat	ggc	ggc	cct	gct	gag	atc	atc	gtg	gac	ggg	2174	
Thr	Ile	Ala	Thr	Cys	His	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Val	Asp	Gly		
				690					695					700			
gta	tct	ggc	ctg	cac	att	gac	cct	tac	cac	agc	gac	aag	gcc	gcg	gat	2222	
Val	Ser	Gly	Leu	His	Ile	Asp	Pro	Tyr	His	Ser	Asp	Lys	Ala	Ala	Asp		
			705					710						715			
atc	ctg	gtc	aac	ttc	ttt	gac	aaa	tgc	aag	gca	gat	ccg	agc	tac	tgg	2270	
Ile	Leu	Val	Asn	Phe	Phe	Asp	Lys	Cys	Lys	Ala	Asp	Pro	Ser	Tyr	Trp		
		720					725					730					
gac	gag	atc	tca	cag	ggc	ggc	ctg	cag	aga	att	tat	gag	aag	tac	acc	2318	
Asp	Glu	Ile	Ser	Gln	Gly	Gly	Leu	Gln	Arg	Ile	Tyr	Glu	Lys	Tyr	Thr		
	735					740					745						
tgg	aag	ctc	tac	tcc	gag	agg	ctg	atg	acc	ctg	acc	ggc	gtg	tac	ggg	2366	
Trp	Lys	Leu	Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu	Thr	Gly	Val	Tyr	Gly		
	750				755					760				765			
ttc	tgg	aag	tac	gtg	agc	aac	ctg	gag	agg	cg	gag	acc	cg	cg	tac	2414	
Phe	Trp	Lys	Tyr	Val	Ser	Asn	Leu	Glu	Arg	Arg	Glu	Thr	Arg	Arg	Tyr		
				770					775					780			
atc	gag	atg	ttc	tac	gcc	ctg	aag	tac	cgt	agc	ctg	gca	agc	cag	gtt	2462	
Ile	Glu	Met	Phe	Tyr	Ala	Leu	Lys	Tyr	Arg	Ser	Leu	Ala	Ser	Gln	Val		
			785					790						795			

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ccg ctg tcc ttc gat tag tacggggaaa gaaggagaag aagaagaaga 2510
Pro Leu Ser Phe Asp *
800

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20 25 30
Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Ala
35 40 45
Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr Ala Pro Phe
50 55 60
Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
65 70 75 80
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
85 90 95
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val Ser Glu Tyr
100 105 110
Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn Ser Asn Phe
115 120 125
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
130 135 140
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
145 150 155 160
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
165 170 175
Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met Met Leu Asn
180 185 190
Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu Arg Lys Ala
195 200 205
Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr Ser Glu Phe
210 215 220
Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
225 230 235 240
Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp Leu Leu Glu
245 250 255
Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
260 265 270
Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
275 280 285
Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
290 295 300
Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
305 310 315 320
Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
325 330 335

Pro	Asp	Ala	Ala	Gly	Thr	Thr	Cys	Gly	Gln	Arg	Leu	Glu	Lys	Val	Ile
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Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu
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Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ser	Ser	Glu	Ile	Met	Lys	Glu	Met	Gln
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Ala	Lys	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val
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Ala	Thr	Leu	Leu	Ala	His	Lys	Leu	Gly	Val	Thr	Gln	Cys	Thr	Ile	Ala
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His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asn	Ser	Asp	Ile	Tyr	Leu	Asp
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Lys	Phe	Asp	Ser	Gln	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr	Ala	Asp	Leu
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Phe	Thr	Leu	Pro	Gly	Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe
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Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met	Ser	Val	Tyr
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Val	Leu	Lys	Asp	Lys	Lys	Lys	Pro	Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu
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Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Tyr	Gly	Lys	Asn
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Ala	Arg	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala	Gly	Asp	His
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Gly	Lys	Glu	Ser	Lys	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Phe	Lys	Lys	Met
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Tyr	Ser	Leu	Ile	Asp	Glu	Tyr	Lys	Leu	Lys	Gly	His	Ile	Arg	Trp	Ile
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Ser	Ala	Gln	Met	Asn	Arg	Val	Arg	Asn	Gly	Glu	Leu	Tyr	Arg	Tyr	Ile
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Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Phe	Tyr	Glu	Ala	Phe
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Gly	Leu	Thr	Val	Ile	Glu	Ser	Met	Thr	Cys	Gly	Leu	Pro	Thr	Ile	Ala
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Phe Asp

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Leu Ser Arg Leu His Ser Val Arg Glu Arg Ile Gly Asp Ser Leu Ser
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gcc cac ccc aat gag ctt gtc gcc gtc ttc acc agg ctg aaa aac ctt 150
Ala His Pro Asn Glu Leu Val Ala Val Phe Thr Arg Leu Lys Asn Leu
30 35 40

gga aag ggt atg ctg cag ccc cac cag atc att gcc gag tac aac aat 198
Gly Lys Gly Met Leu Gln Pro His Gln Ile Ile Ala Glu Tyr Asn Asn
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gcg atc cct gag gct gag cgc gag aag ctc aag gat ggt gct ttt gag 246
Ala Ile Pro Glu Ala Glu Arg Glu Lys Leu Lys Asp Gly Ala Phe Glu
60 65 70

gat gtc ctg agg gca gct cag gag gcg att gtc atc ccc cca tgg gtt 294
Asp Val Leu Arg Ala Ala Gln Glu Ala Ile Val Ile Pro Pro Trp Val
75 80 85

gca ctt gcc atc cgc cct agg cct ggt gtc tgg gag tat gtg agg gtc 342
Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val
90 95 100 105

aac gtc agt gag ctc gct gtt gag gag ctg aga gtt cct gag tac ctg 390
Asn Val Ser Glu Leu Ala Val Glu Glu Leu Arg Val Pro Glu Tyr Leu
110 115 120

cag ttc aag gaa cag ctt gtg gaa gaa ggc ccc aac aac aac ttt gtt 438
Gln Phe Lys Glu Gln Leu Val Glu Glu Gly Pro Asn Asn Asn Phe Val
125 130 135

ctt gag ctg gac ttt gag cca ttc aat gcc tcc ttc ccc cgt cct tct 486
Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro Ser
140 145 150

ctg tca aag tcc att ggc aat ggc gtg cag ttc ctc aac agg cac ctg 534
Leu Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu
155 160 165

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tca tca aag ctc ttc cat gac aag gag agc atg tac ccc ttg ctc aac Ser Ser Lys Leu Phe His Asp Lys Glu Ser Met Tyr Pro Leu Leu Asn 170 175 180 185	582
ttc ctt cgc gcc cac aac tac aag ggg atg acc atg atg ttg aac gac Phe Leu Arg Ala His Asn Tyr Lys Gly Met Thr Met Met Leu Asn Asp 190 195 200	630
aga atc cgc agt ctc agt gct ctg caa ggt gcg ctg agg aag gct gag Arg Ile Arg Ser Leu Ser Ala Leu Gln Gly Ala Leu Arg Lys Ala Glu 205 210 215	678
gag cac ctg tcc acc cta caa gct gat acc cca tac tct gaa ttt cac Glu His Leu Ser Thr Leu Gln Ala Asp Thr Pro Tyr Ser Glu Phe His 220 225 230	726
cac agg ttc cag gaa ctt ggt ctg gag aag ggt tgg ggt gat tgc gct His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Cys Ala 235 240 245	774
aag cgt gca cag gag act atc cac ctc ctc ttg gac ctc ctg gag gcc Lys Arg Ala Gln Glu Thr Ile His Leu Leu Leu Asp Leu Leu Glu Ala 250 255 260 265	822
cca gat ccg tcc acc ctg gag aag ttc ctt gga acg atc ccc atg gtg Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Thr Ile Pro Met Val 270 275 280	870
ttc aat gtc gtt atc ctc tcc cct cat ggt tac ttc gct caa gct aat Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ala Asn 285 290 295	918
gtc ttg ggt tac cct gac acc gga ggc cag gtt gtc tac atc ttg gat Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu Asp 300 305 310	966
caa gtg cgc gct atg gag aac gaa atg ctg ctg agg atc aag cag tgt Gln Val Arg Ala Met Glu Asn Glu Met Leu Leu Arg Ile Lys Gln Cys 315 320 325	1014
ggg ctt gac atc acg ccg aag atc ctt att gtc acc agg ttg ctc cct Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu Pro 330 335 340 345	1062
gat gca act ggc acc acc tgt ggc cag cgc ctt gag aag gtc ctt ggc Asp Ala Thr Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Leu Gly 350 355 360	1110
acc gag cac tgc cat atc ctt cgc gtg cca ttc aga aca gaa aac gga Thr Glu His Cys His Ile Leu Arg Val Pro Phe Arg Thr Glu Asn Gly 365 370 375	1158
atc gtt cgc aag tgg atc tcg cga ttt gaa gtc tgg ccg tac ctg gag Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp Pro Tyr Leu Glu 380 385 390	1206
act tac act gat gac gtg gcg cat gag att gct gga gag ctt cag gcc Thr Tyr Thr Asp Asp Val Ala His Glu Ile Ala Gly Glu Leu Gln Ala	1254

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tgt ttg ctc gcc cac aag atg ggt gtt act cac tgt acc att gcc cat Cys Leu Leu Ala His Lys Met Gly Val Thr His Cys Thr Ile Ala His 430 435 440			1350
gcg ctt gag aaa act aag tac cct aac tcc gac ctc tac tgg aag aag Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Leu Tyr Trp Lys Lys 445 450 455			1398
ttt gag gat cac tac cac ttc tcg tgc cag ttc acc act gac ttg att Phe Glu Asp His Tyr His Phe Ser Cys Gln Phe Thr Thr Asp Leu Ile 460 465 470			1446
gca atg aac cat gcc gac ttc atc atc acc agt acc ttc caa gag atc Ala Met Asn His Ala Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu Ile 475 480 485			1494
gcc gga aac aag gac acc gtc ggc cag tac gag tca cac atg gcg ttc Ala Gly Asn Lys Asp Thr Val Gly Gln Tyr Glu Ser His Met Ala Phe 490 495 500 505			1542
aca atg cct ggc ctg tac cgc gtt gtc cac ggc att gat gtg ttc gac Thr Met Pro Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp 510 515 520			1590
ccc aag ttc aac atc gtg tct cct ggc gcg gac ctg tcc atc tac ttc Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Leu Ser Ile Tyr Phe 525 530 535			1638
ccg tac acc gag tcg cac aag agg ctg acc tcc ctt cac ccg gag att Pro Tyr Thr Glu Ser His Lys Arg Leu Thr Ser Leu His Pro Glu Ile 540 545 550			1686
gag gag ctc ctg tac agc caa acc gag aac acg gag cac aag ttc gtt Glu Glu Leu Leu Tyr Ser Gln Thr Glu Asn Thr Glu His Lys Phe Val 555 560 565			1734
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cgt gtg aag aac ttg act ggg ctg gtg gag ctg tac ggc cgg aac aag Arg Val Lys Asn Leu Thr Gly Leu Val Glu Leu Tyr Gly Arg Asn Lys 590 595 600			1830
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aac cct tcc aag gac aag gag gag cag gcc gag ttc aag aag atg ttt Asn Pro Ser Lys Asp Lys Glu Glu Gln Ala Glu Phe Lys Lys Met Phe 620 625 630			1926

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gac acc aag ggc gcc ttc gtg cag cct gct ttc tac gag gct ttc ggg Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe Gly 670 675 680	2070
ctg acg gtg gtt gag gcc atg acc tgc ggc ctg ccc acg ttc gcc acc Leu Thr Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr 685 690 695	2118
gcc tac ggc ggt ccg gcc gag atc atc gtg cac ggc gtg tct ggc tac Ala Tyr Gly Gly Pro Ala Glu Ile Ile Val His Gly Val Ser Gly Tyr 700 705 710	2166
cac atc gac cct tac cag ggc gac aag gcg tcg gcc ctg ctc gtg gac His Ile Asp Pro Tyr Gln Gly Asp Lys Ala Ser Ala Leu Leu Val Asp 715 720 725	2214
ttc ttc gac aag tgc cag gcg gag ccg agc cac tgg agc aag atc tcc Phe Phe Asp Lys Cys Gln Ala Glu Pro Ser His Trp Ser Lys Ile Ser 730 735 740 745	2262
cag ggc ggg ctc cag cgt atc gag gag aag tac acc tgg aag ctg tac Gln Gly Gly Leu Gln Arg Ile Glu Glu Lys Tyr Thr Trp Lys Leu Tyr 750 755 760	2310
tcg gag agg ctg atg acc ctc acc ggc gtg tac ggg ttc tgg aag tac Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys Tyr 765 770 775	2358
gtg tcc aac ctg gag agg cgc gag acc cgg cgg tac ctg gag atg ctg Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met Leu 780 785 790	2406
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gag gga gag ccc tcc agc aag tga tgcgtgacgg cggccacaga cctgatcgat Glu Gly Glu Pro Ser Ser Lys * 810 815	2508
cgatgagcga gagggagcac tcggagtgtc gtgtcttttc ccttgccatt tctttctttc	2568
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cattgatccg ggtgtcgctt gtagtagtct gatggactgt tagtagtttg cgttgcgtcg	2748
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ttcctggatg ggatgttgct ccttgaataa taatcgtagt ggccttgag cccttttcct	2868
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 Ala Val Phe Thr Arg Leu Lys Asn Leu Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Ile Ala Glu Tyr Asn Asn Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
 100 105 110
 Glu Glu Leu Arg Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Glu Glu Gly Pro Asn Asn Asn Phe Val Leu Glu Leu Asp Phe Glu Pro
 130 135 140
 Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn
 145 150 155 160
 Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp
 165 170 175
 Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
 180 185 190
 Lys Gly Met Thr Met Met Leu Asn Asp Arg Ile Arg Ser Leu Ser Ala
 195 200 205
 Leu Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Thr Leu Gln
 210 215 220
 Ala Asp Thr Pro Tyr Ser Glu Phe His His Arg Phe Gln Glu Leu Gly
 225 230 235 240
 Leu Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Ile
 245 250 255
 His Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu
 260 265 270
 Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser
 275 280 285
 Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr
 290 295 300
 Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn
 305 310 315 320
 Glu Met Leu Leu Arg Ile Lys Gln Cys Gly Leu Asp Ile Thr Pro Lys
 325 330 335
 Ile Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys
 340 345 350
 Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Cys His Ile Leu
 355 360 365
 Arg Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser
 370 375 380
 Arg Phe Glu Val Trp Pro Tyr Leu Glu Thr Tyr Thr Asp Asp Val Ala
 385 390 395 400
 His Glu Ile Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly
 405 410 415
 Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met
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Ser	Cys	Gln	Phe	Thr	Thr	Asp	Leu	Ile	Ala	Met	Asn	His	Ala	Asp	Phe
465					470					475					480
Ile	Ile	Thr	Ser	Thr	Phe	Gln	Glu	Ile	Ala	Gly	Asn	Lys	Asp	Thr	Val
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Gly	Gln	Tyr	Glu	Ser	His	Met	Ala	Phe	Thr	Met	Pro	Gly	Leu	Tyr	Arg
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Val	Val	His	Gly	Ile	Asp	Val	Phe	Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser
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Thr	Glu	Asn	Thr	Glu	His	Lys	Phe	Val	Leu	Asn	Asp	Arg	Asn	Lys	Pro
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Leu	Val	Glu	Leu	Tyr	Gly	Arg	Asn	Lys	Arg	Leu	Gln	Glu	Leu	Val	Asn
		595					600					605			
Leu	Val	Val	Val	Cys	Gly	Asp	His	Gly	Asn	Pro	Ser	Lys	Asp	Lys	Glu
	610				615						620				
Glu	Gln	Ala	Glu	Phe	Lys	Lys	Met	Phe	Asp	Leu	Ile	Glu	Gln	Tyr	Asn
625					630					635					640
Leu	Asn	Gly	His	Ile	Arg	Trp	Ile	Ser	Ala	Gln	Met	Asn	Arg	Val	Arg
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Asn	Gly	Glu	Leu	Tyr	Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val
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Gln	Pro	Ala	Phe	Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met
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Thr	Cys	Gly	Leu	Pro	Thr	Phe	Ala	Thr	Ala	Tyr	Gly	Gly	Pro	Ala	Glu
	690				695						700				
Ile	Ile	Val	His	Gly	Val	Ser	Gly	Tyr	His	Ile	Asp	Pro	Tyr	Gln	Gly
705					710					715					720
Asp	Lys	Ala	Ser	Ala	Leu	Leu	Val	Asp	Phe	Phe	Asp	Lys	Cys	Gln	Ala
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Glu	Pro	Ser	His	Trp	Ser	Lys	Ile	Ser	Gln	Gly	Gly	Leu	Gln	Arg	Ile
			740					745					750		
Glu	Glu	Lys	Tyr	Thr	Trp	Lys	Leu	Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu
		755					760					765			
Thr	Gly	Val	Tyr	Gly	Phe	Trp	Lys	Tyr	Val	Ser	Asn	Leu	Glu	Arg	Arg
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gag gac acc ctc cac gcg cac cgc aac gag ctc gtc gcc ctc ctc tcc   96
Glu Asp Thr Leu His Ala His Arg Asn Glu Leu Val Ala Leu Leu Ser
             20             25             30

aag tac gtg aac aag ggg aag ggc atc ctg cag ccg cac cac atc ctc   144
Lys Tyr Val Asn Lys Gly Lys Gly Ile Leu Gln Pro His His Ile Leu
             35             40             45

gac gcg ctc gac gag gtc cag ggc tcc ggg gtc cgc gcg ctc gcc gag   192
Asp Ala Leu Asp Glu Val Gln Gly Ser Gly Val Arg Ala Leu Ala Glu
             50             55             60

gga ccc ttc ctc gac gtc ctc cgc tcc gcg cag gag gcg atc gtg ctg   240
Gly Pro Phe Leu Asp Val Leu Arg Ser Ala Gln Glu Ala Ile Val Leu
             65             70             75             80

ccg ccg ttc gtg gcc atc gcg gtg cgc ccg cgc ccg gga gtt tgg gag   288
Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu

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tcg	gag	tac	ctc	cgc	ttc	aag	gag	gag	ctt	gtc	gac	ggc	cag	cac	aat	384				
Ser	Glu	Tyr	Leu	Arg	Phe	Lys	Glu	Glu	Leu	Val	Asp	Gly	Gln	His	Asn					
115				120				125												
gat	ccc	tac	gtt	ctc	gag	ctt	gac	ttc	gag	ccg	ttc	aat	gtc	tca	gtc	432				
Asp	Pro	Tyr	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Val	Ser	Val					
130				135				140												
cca	cgc	cca	aat	cgg	tca	tca	tct	att	gga	aac	ggg	gtg	cag	ttc	ctc	480				
Pro	Arg	Pro	Asn	Arg	Ser	Ser	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu					
145				150				155				160								
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Asn	Arg	His	Leu	Ser	Ser	Ile	Met	Phe	Arg	Asn	Arg	Asp	Cys	Leu	Glu					
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ccc	ctg	ttg	gat	ttc	ctc	cgt	ggc	cac	cgg	cac	aag	ggg	cat	gtt	atg	576				
Pro	Leu	Leu	Asp	Phe	Leu	Arg	Gly	His	Arg	His	Lys	Gly	His	Val	Met					
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atg	ctt	aat	gat	aga	ata	caa	agc	ttg	ggg	agg	ctt	cag	tct	gtg	ctg	624				
Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Gly	Arg	Leu	Gln	Ser	Val	Leu					
195				200				205												
acc	aaa	gct	gag	gag	cac	ttg	tca	aag	ctc	cct	gct	gac	aca	cca	tac	672				
Thr	Lys	Ala	Glu	Glu	His	Leu	Ser	Lys	Leu	Pro	Ala	Asp	Thr	Pro	Tyr					
210				215				220												
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Ser	Gln	Phe	Ala	Tyr	Lys	Phe	Gln	Glu	Trp	Gly	Leu	Glu	Lys	Gly	Trp					
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Ile	Pro	Met	Ile	Phe	Asn	Val	Val	Val	Val	Ser	Pro	His	Gly	Tyr	Phe					
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Leu Lys Lys Gln Gly Leu Asp Val Ser Pro Lys Ile Leu Ile Val Thr	
325 330 335	
cgg ctg ata cca gat gca aaa gga aca tca tgc aat cag cgg ctt gag	1056
Arg Leu Ile Pro Asp Ala Lys Gly Thr Ser Cys Asn Gln Arg Leu Glu	
340 345 350	
aga att agt gga aca cag cat act tac ata tta cga gtt ccc ttc aga	1104
Arg Ile Ser Gly Thr Gln His Thr Tyr Ile Leu Arg Val Pro Phe Arg	
355 360 365	
aat gaa aat ggg ata ctt aag aaa tgg ata tca aga ttt gat gtg tgg	1152
Asn Glu Asn Gly Ile Leu Lys Lys Trp Ile Ser Arg Phe Asp Val Trp	
370 375 380	
cca tat ctg gaa aca ttt gct gag gat gct gct ggt gaa att gct gct	1200
Pro Tyr Leu Glu Thr Phe Ala Glu Asp Ala Ala Gly Glu Ile Ala Ala	
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gaa tta caa ggt act cca gac ttc ata att gga aac tac agt gat gga	1248
Glu Leu Gln Gly Thr Pro Asp Phe Ile Ile Gly Asn Tyr Ser Asp Gly	
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aat ctt gtg gcg tca ttg cta tct tac aag atg gga att acc cag tgc	1296
Asn Leu Val Ala Ser Leu Leu Ser Tyr Lys Met Gly Ile Thr Gln Cys	
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aac att gct cat gct ctg gaa aag act aag tat cca gat tca gac ata	1344
Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile	
435 440 445	
ttt tgg aag aat ttc gat gag aag tac cat ttc tcc tgc cag ttc act	1392
Phe Trp Lys Asn Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr	
450 455 460	
gct gat ata att gct atg aac aat gct gat ttt atc atc acc agc aca	1440
Ala Asp Ile Ile Ala Met Asn Asn Ala Asp Phe Ile Ile Thr Ser Thr	
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Tyr Gln Glu Ile Ala Gly Ser Lys Asn Thr Val Gly Gln Tyr Glu Ser	
485 490 495	
cat act gcc ttt act ctg cct ggt ctg tac cga gtt gtc cat ggg atc	1536
His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile	
500 505 510	
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Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met	
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tcc ata tac ttt cca cat acc gag aag gcc aag cga ctc acc tct ctt	1632
Ser Ile Tyr Phe Pro His Thr Glu Lys Ala Lys Arg Leu Thr Ser Leu	
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cat ggt tca atc gaa aat ttg att tat gac ccg gag caa aac gat gaa	1680
His Gly Ser Ile Glu Asn Leu Ile Tyr Asp Pro Glu Gln Asn Asp Glu	

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cac att ggg cat ctg gat gac cgg tca aag ccc atc ctc ttc tcc atg	1728			
His Ile Gly His Leu Asp Asp Arg Ser Lys Pro Ile Leu Phe Ser Met				
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Ala Arg Leu Asp Arg Val Lys Asn Ile Thr Gly Leu Val Glu Ala Phe				
580	585	590		
gct aag tgc gct aag ctg agg gag ctg gta aac ctt gtc gtc gtt gcc	1824			
Ala Lys Cys Ala Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Ala				
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ggg tac aat gat gtc aac aag tcc aag gac agg gaa gag atc gcg gag	1872			
Gly Tyr Asn Asp Val Asn Lys Ser Lys Asp Arg Glu Glu Ile Ala Glu				
610	615	620		
ata gag aag atg cat gaa ctc atc aag acc cac aac ttg ttc ggg cag	1920			
Ile Glu Lys Met His Glu Leu Ile Lys Thr His Asn Leu Phe Gly Gln				
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Phe Arg Trp Ile Ser Ala Gln Thr Asn Arg Ala Arg Asn Gly Glu Leu				
645	650	655		
tat cgc tac atc gct gat acc cat ggt gct ttc gta cag ccg gcc ttg	2016			
Tyr Arg Tyr Ile Ala Asp Thr His Gly Ala Phe Val Gln Pro Ala Leu				
660	665	670		
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Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu				
675	680	685		
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Pro Thr Phe Ala Thr Leu His Gly Gly Pro Ala Glu Ile Ile Glu His				
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ggc gtc tcg ggc ttc cac att gac ccg tac cac ccc gaa cag gct gtt	2160			
Gly Val Ser Gly Phe His Ile Asp Pro Tyr His Pro Glu Gln Ala Val				
705	710	715	720	
aat ctg atg gcc gac ttc ttc gac cgg tgc aag caa gac cca gat cac	2208			
Asn Leu Met Ala Asp Phe Phe Asp Arg Cys Lys Gln Asp Pro Asp His				
725	730	735		
tgg gtg aat ata tct gga gca ggg ctg cag cgc ata tac gag aag tac	2256			
Trp Val Asn Ile Ser Gly Ala Gly Leu Gln Arg Ile Tyr Glu Lys Tyr				
740	745	750		
aca tgg aag ata tac tca gag agg ttg atg aca ctg gcc ggg gtc tac	2304			
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Met Thr Leu Ala Gly Val Tyr				
755	760	765		
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Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg				
770	775	780		

tac ctt gag atg ttc tac ata ctg aag ttc cgc gag ctg gcg aag acc 2400
 Tyr Leu Glu Met Phe Tyr Ile Leu Lys Phe Arg Glu Leu Ala Lys Thr
 785 790 795 800

gtg ccg ctt gca att gac caa ccg cag tag cttgcgcaac tgcgactgcg 2450
 Val Pro Leu Ala Ile Asp Gln Pro Gln *
 805

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			20					25					30		
Lys	Tyr	Val	Asn	Lys	Gly	Lys	Gly	Ile	Leu	Gln	Pro	His	His	Ile	Leu
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Asp	Ala	Leu	Asp	Glu	Val	Gln	Gly	Ser	Gly	Val	Arg	Ala	Leu	Ala	Glu
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Pro	Pro	Phe	Val	Ala	Ile	Ala	Val	Arg	Pro	Arg	Pro	Gly	Val	Trp	Glu
				85					90					95	
Tyr	Val	Arg	Val	Asn	Val	His	Glu	Leu	Ser	Val	Glu	Gln	Leu	Thr	Val
			100					105					110		
Ser	Glu	Tyr	Leu	Arg	Phe	Lys	Glu	Glu	Leu	Val	Asp	Gly	Gln	His	Asn
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Asp	Pro	Tyr	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Val	Ser	Val
		130					135				140				
Pro	Arg	Pro	Asn	Arg	Ser	Ser	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu
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Asn	Arg	His	Leu	Ser	Ser	Ile	Met	Phe	Arg	Asn	Arg	Asp	Cys	Leu	Glu
			165						170					175	
Pro	Leu	Leu	Asp	Phe	Leu	Arg	Gly	His	Arg	His	Lys	Gly	His	Val	Met
			180					185					190		
Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Gly	Arg	Leu	Gln	Ser	Val	Leu
		195					200					205			
Thr	Lys	Ala	Glu	Glu	His	Leu	Ser	Lys	Leu	Pro	Ala	Asp	Thr	Pro	Tyr
	210				215						220				
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225					230					235				240	
Gly	Asp	Thr	Ala	Gly	His	Val	Leu	Glu	Met	Ile	His	Leu	Leu	Leu	Asp
				245					250					255	
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Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Val	Leu	Arg
305					310					315					320
Leu	Lys	Lys	Gln	Gly	Leu	Asp	Val	Ser	Pro	Lys	Ile	Leu	Ile	Val	Thr
				325					330					335	
Arg	Leu	Ile	Pro	Asp	Ala	Lys	Gly	Thr	Ser	Cys	Asn	Gln	Arg	Leu	Glu
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Arg	Ile	Ser	Gly	Thr	Gln	His	Thr	Tyr	Ile	Leu	Arg	Val	Pro	Phe	Arg
		355					360					365			
Asn	Glu	Asn	Gly	Ile	Leu	Lys	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp
		370				375					380				
Pro	Tyr	Leu	Glu	Thr	Phe	Ala	Glu	Asp	Ala	Ala	Gly	Glu	Ile	Ala	Ala
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Glu	Leu	Gln	Gly	Thr	Pro	Asp	Phe	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly
				405					410					415	
Asn	Leu	Val	Ala	Ser	Leu	Leu	Ser	Tyr	Lys	Met	Gly	Ile	Thr	Gln	Cys
			420					425					430		
Asn	Ile	Ala	His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asp	Ser	Asp	Ile
		435						440				445			
Phe	Trp	Lys	Asn	Phe	Asp	Glu	Lys	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr
		450				455					460				
Ala	Asp	Ile	Ile	Ala	Met	Asn	Asn	Ala	Asp	Phe	Ile	Ile	Thr	Ser	Thr
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Tyr	Gln	Glu	Ile	Ala	Gly	Ser	Lys	Asn	Thr	Val	Gly	Gln	Tyr	Glu	Ser
				485					490					495	
His	Thr	Ala	Phe	Thr	Leu	Pro	Gly	Leu	Tyr	Arg	Val	Val	His	Gly	Ile
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Asp	Val	Phe	Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met
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Ser	Ile	Tyr	Phe	Pro	His	Thr	Glu	Lys	Ala	Lys	Arg	Leu	Thr	Ser	Leu
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His	Ile	Gly	His	Leu	Asp	Asp	Arg	Ser	Lys	Pro	Ile	Leu	Phe	Ser	Met
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Ala	Arg	Leu	Asp	Arg	Val	Lys	Asn	Ile	Thr	Gly	Leu	Val	Glu	Ala	Phe
			580					585					590		
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		610				615					620				
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Phe	Arg	Trp	Ile	Ser	Ala	Gln	Thr	Asn	Arg	Ala	Arg	Asn	Gly	Glu	Leu
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Tyr	Arg	Tyr	Ile	Ala	Asp	Thr	His	Gly	Ala	Phe	Val	Gln	Pro	Ala	Leu
			660					665					670		
Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met	Thr	Cys	Gly	Leu
		675					680					685			
Pro	Thr	Phe	Ala	Thr	Leu	His	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Glu	His
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 Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg
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